#8/a

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: MAKISHIMA, FUSAO; TAKAMATSU, HIROYUKI; MIKI, HIDEO; KAWAI, SHINJI; KIMURA, MICHIO; MATSUMOTO, TOMOAKI; KATSUURA, MIEKO; ENOMOTO, KOICHI; SATOH, YUSUKE

(ii) TITLE OF INVENTION: A NOVEL PROTEIN AND PROCESS FOR PREPARING THE SAME

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BIERMAN, MUSERLIAN AND LUCAS LLP
(B) STREET: 600 THIRD AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10016

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: MICROSOFT WORD 97

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/945,459
(B) FILING DATE: 09-DEC-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/JP96/01062
(B) FILING DATE: 19-APR-1996

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP7/322403
(B) FILING DATE: 17-NOV-1995

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP7/93664
(B) FILING DATE: 19-APR-1995

(vii) ATTORNEY/AGENT INFORMATION:

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS:
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:
(A) ORGANISM: HOMOSAPIENS
(F) TISSUE TYPE: FETUS

(ix) FEATURE:
(A) NAME/KEY: MP52
(B) LOCATION: 383 TO 501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys
1               5                  10

Asn Leu Lys Ala Arg Cys Ser Arg Lys Ala Leu His
        15                  20

Val Asn Phe Lys Asp Met Gly Trp Asp Asp Trp Ile
 25                  30                  35

Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
            40                  45

Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu
     50                  55                  60

Pro Thr Asn His Ala Val Ile Gln Thr Leu Met Asn
                65                  70
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Ser Met Asp Pro Glu Ser Thr Pro Pro Thr Cys Cys
75 80

Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
85 90 95

Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr
100 105

Glu Asp Met Val Val Glu Ser Cys Gly Cys Arg
110 115

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATAATGCCAC TAGCAACTCG TCAGGGC 27

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGTCGACTAC CTGCAGCCAC ACGACT 26

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 357 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CCA CTG GCC ACT CGC CAG GGC AAG CGA CCC AGC AAG                    36
Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys
1               5                  10

AAC CTT AAG GCT CGC TGC AGT CGG AAG GCA CTG CAT                    72
Asn Leu Lys Ala Arg Cys Ser Arg Lys Ala Leu His
        15                  20

GTC AAC TTC AAG GAC ATG GGC TGG GAC GAC TGG ATC                   108
Val Asn Phe Lys Asp Met Gly Trp Asp Asp Trp Ile
 25                  30                  35

ATC GCA CCC CTT GAG TAC GAG GCT TTC CAC TGC GAG                   144
Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
            40                  45

GGG CTG TGC GAG TTC CCA TTG CGC TCC CAC CTG GAG                   180
Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu
     50                  55                  60

CCC ACG AAT CAT GCA GTC ATC CAG ACC CTG ATG AAC                   216
Pro Thr Asn His Ala Val Ile Gln Thr Leu Met Asn
                65                  70

TCC ATG GAC CCC GAG TCC ACA CCA CCC ACC TGC TGT                   252
Ser Met Asp Pro Glu Ser Thr Pro Pro Thr Cys Cys
        75                  80

GTG CCC ACG CGA CTG AGT CCC ATC AGC ATC CTC TTC                   288
Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
 85                  90                  95

ATT GAC TCT GCC AAC AAC GTG GTG TAT AAG CAG TAT                   324
Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr
            100                 105

GAG GAC ATG GTC GTG GAG TCG TGT GGC TGC AGG                       357
Glu Asp Met Val Val Glu Ser Cys Gly Cys Arg
    110                 115
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